CLAIMS

We claim:

1. A method for generating a secondary library of scaffold protein variants comprising:

a) receiving a library of primary sequences generated utilizing an alignment program;

b) generating a probability distribution table of amino acid residues in a plurality of variant positions from said primary sequences;

c) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences; and

d) computationally ranking said secondary library.

2. A method according to claim 1, wherein said alignment program is a sequence alignment program.

3. A method according to claim 1, wherein said alignment program is a structural alignment program.

4. A method according to claim 1 further comprising synthesizing a plurality of said secondary sequences.

5. A method according to claim 4 wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.

6. A method according to 5 wherein said pooled oligonucleotides are added in equimolar amounts.

7. A method according to claim 5 wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the mutation.

8. A method according to claim 6 wherein said pooled oligonucleotides are pooled in relative amounts.